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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/596,444	06/19/2000	Wei Huang	LJL 354B	4000

7590 01/09/2002

Kolisch Hartwell Dickinson McCormack & Heuser
James R Abney
520 S W Yamhill Street
Suite 200
Portland, OR 97204

EXAMINER	
GABEL, GAILENE	
ART UNIT	PAPER NUMBER
1641	9

DATE MAILED: 01/09/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
09/596,444	6/19/00	HUANG et al.	LJL 354B

EXAMINER	
Gailene R. Gabel	
ART UNIT	**PAPER**
1641	9

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

The communication filed **05 October 2001** is not fully responsive to the Office communication mailed **31 August 2001** for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner **Gailene R. Gabel**, Art Unit **1641**, whose telephone number is (703) 305-0807.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

Christopher L. Chin

CHRISTOPHER L. CHIN
PRIMARY EXAMINER
GROUP ~~1800~~ 1641

Gailene R. Gabel
12/8/01

Notice to Comply	Application No.	Applicant(s)	
	09/596,444	HUANG *et al.*	
	Examiner	Art Unit	
	Gabel	1641	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

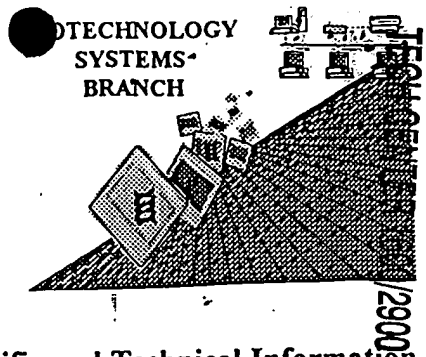
☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY



RAW SEQUENCE LISTING ERROR REPORT

3617

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/596,444

Source: AU 1600

Date Processed by STIC: 10/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/596,444

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequen <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknow is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rule
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	'n' can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to repre any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RECEIVED

NOV 1 3 2001

GROUP 3600

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

1600

RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

```
  3 <110> APPLICANT: Huang, Wei
  4       Hoekstra, Merl F
  5       Lee, Sandra K
  6       Cairns, Nicholas
  7       Kauvar, Lawrence M
  8       Sportsman, J Richard
 10 <120> TITLE OF INVENTION: PHOSPHORYLATION ASSAYS
 12 <130> FILE REFERENCE: LJL 354B
 14 <140> CURRENT APPLICATION NUMBER: US 09/596,444
 15 <141> CURRENT FILING DATE: 2000-06-19
 17 <160> NUMBER OF SEQ ID NOS: 48
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 10
 23 <212> TYPE: PRT
C--> 24 <213> ORGANISM: Artificial
 26 <220> FEATURE:
 27 <221> NAME/KEY: MOD_RES
 28 <222> LOCATION: (5)..(5)
 29 <223> OTHER INFORMATION: PHOSPHORYLATION
 32 <220> FEATURE:
 33 <221> NAME/KEY: MOD_RES
 34 <222> LOCATION: (10)..(10)
 35 <223> OTHER INFORMATION: BIOTINYLATION
 38 <400> SEQUENCE: 1
 40 Gly Glu Glu Gly Tyr Met Pro Met Gly Lys
 41 1               5                  10
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 17
 46 <212> TYPE: PRT
C--> 47 <213> ORGANISM: Artificial
 49 <220> FEATURE:
 50 <221> NAME/KEY: MOD_RES
 51 <222> LOCATION: (1)..(1)
 52 <223> OTHER INFORMATION: BIOTINYLATION
 55 <220> FEATURE:
 56 <221> NAME/KEY: MOD_RES
 57 <222> LOCATION: (1)..(1)
 58 <223> OTHER INFORMATION: AMIDATION
 61 <400> SEQUENCE: 2
 63 Glu Gly Pro Trp Leu Glu Glu Glu Glu Glu Ala Tyr Gly Trp Met Asp
 64 1               5                  10                  15
 67 Phe
 71 <210> SEQ ID NO: 3
 72 <211> LENGTH: 8
 73 <212> TYPE: PRT
C--> 74 <213> ORGANISM: Artificial
```

Does Not Comply
Corrected Diskette Needed

Errored: A 213 response of "Artificial" requires an explanation in Field 223.
FYI: "Artificial Sequence" is the preferred response. mm

A Field 223 explanation is mandatory

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

W--> 76 <220> FEATURE:
W--> 76 <223> OTHER INFORMATION:
76 <400> SEQUENCE: 3
78 Asp Tyr Met Thr Met Gln Ile Gly
79 1 5
82 <210> SEQ ID NO: 4
83 <211> LENGTH: 11
84 <212> TYPE: PRT
C--> 85 <213> ORGANISM: Artificial
W--> 87 <220> FEATURE:
W--> 87 <223> OTHER INFORMATION:
87 <400> SEQUENCE: 4
89 Ser Arg Gly Asp Tyr Met Thr Met Gln Ile Gly
90 1 5 10
93 <210> SEQ ID NO: 5
94 <211> LENGTH: 11
95 <212> TYPE: PRT
C--> 96 <213> ORGANISM: Artificial
W--> 98 <220> FEATURE:
W--> 98 <223> OTHER INFORMATION:
98 <400> SEQUENCE: 5
100 Glu Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu
101 1 5 10
104 <210> SEQ ID NO: 6
105 <211> LENGTH: 10
106 <212> TYPE: PRT
C--> 107 <213> ORGANISM: Artificial
109 <220> FEATURE:
110 <221> NAME/KEY: MOD_RES
111 <222> LOCATION: (5)..(5)
112 <223> OTHER INFORMATION: PHOSPHORYLATION
115 <400> SEQUENCE: 6
117 Glu Lys Arg Pro Ser Arg Ser Lys Tyr Leu
118 1 5 10
121 <210> SEQ ID NO: 7
122 <211> LENGTH: 10
123 <212> TYPE: PRT
C--> 124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <221> NAME/KEY: MOD_RES
128 <222> LOCATION: (8)..(8)
129 <223> OTHER INFORMATION: PHOSPHORYLATION
132 <400> SEQUENCE: 7
134 Glu Lys Arg Pro Ser Gln Arg Ser Tyr Leu
135 1 5 10
138 <210> SEQ ID NO: 8
139 <211> LENGTH: 9
140 <212> TYPE: PRT
C--> 141 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

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     144 <221> NAME/KEY: MOD_RES
     145 <222> LOCATION: (5)..(5)
     146 <223> OTHER INFORMATION: PHOSPHORYLATION
     149 <220> FEATURE:
     150 <221> NAME/KEY: MOD_RES
     151 <222> LOCATION: (7)..(7)
     152 <223> OTHER INFORMATION: PHOSPHORYLATION
     155 <400> SEQUENCE: 8
     157 Glu Lys Arg Pro Ser Arg Ser Tyr Leu
     158 1               5
     161 <210> SEQ ID NO: 9
     162 <211> LENGTH: 14
     163 <212> TYPE: PRT
C--> 164 <213> ORGANISM: Artificial
     166 <220> FEATURE:
     167 <221> NAME/KEY: MOD_RES
     168 <222> LOCATION: (11)..(11)
     169 <223> OTHER INFORMATION: PHOSPHORYLATION
     172 <400> SEQUENCE: 9
     174 Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg Lys
     175 1               5                   10
     178 <210> SEQ ID NO: 10
     179 <211> LENGTH: 11
     180 <212> TYPE: PRT
C--> 181 <213> ORGANISM: Artificial
     183 <220> FEATURE:
     184 <221> NAME/KEY: MOD_RES
     185 <222> LOCATION: (7)..(7)
     186 <223> OTHER INFORMATION: PHOSPHORYLATION
     189 <400> SEQUENCE: 10
     191 Lys His Phe Pro Gln Phe Ser Tyr Ser Ala Ser
     192 1               5                   10
     195 <210> SEQ ID NO: 11
     196 <211> LENGTH: 11
     197 <212> TYPE: PRT
C--> 198 <213> ORGANISM: Artificial
     200 <220> FEATURE:
     201 <221> NAME/KEY: MOD_RES
     202 <222> LOCATION: (1)..(1)
     203 <223> OTHER INFORMATION: PHOSPHORYLATION
     206 <400> SEQUENCE: 11
     208 Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln Cys
     209 1               5                   10
     212 <210> SEQ ID NO: 12
     213 <211> LENGTH: 11
     214 <212> TYPE: PRT
C--> 215 <213> ORGANISM: Artificial
     217 <220> FEATURE:
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RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

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     218 <221> NAME/KEY: MOD_RES
     219 <222> LOCATION: (9)..(9)
     220 <223> OTHER INFORMATION: PHOSPHORYLATION
     223 <220> FEATURE:
     224 <221> NAME/KEY: MOD_RES
     225 <222> LOCATION: (11)..(11)
     226 <223> OTHER INFORMATION: PHOSPHORYLATION
     229 <400> SEQUENCE: 12
     231 Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
     232 1               5                   10
     235 <210> SEQ ID NO: 13
     236 <211> LENGTH: 11
     237 <212> TYPE: PRT
C--> 238 <213> ORGANISM: Artificial
     240 <220> FEATURE:
     241 <221> NAME/KEY: MOD_RES
     242 <222> LOCATION: (6)..(6)
     243 <223> OTHER INFORMATION: PHOSPHORYLATION
     246 <400> SEQUENCE: 13
     248 Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
     249 1               5                   10
     252 <210> SEQ ID NO: 14
     253 <211> LENGTH: 5
     254 <212> TYPE: PRT
C--> 255 <213> ORGANISM: Artificial
     257 <220> FEATURE:
     258 <221> NAME/KEY: MOD_RES
     259 <222> LOCATION: (2)..(2)
     260 <223> OTHER INFORMATION: PHOSPHORYLATION
     263 <400> SEQUENCE: 14
     265 Leu Thr Pro Leu Lys
     266 1               5
     269 <210> SEQ ID NO: 15
     270 <211> LENGTH: 5
     271 <212> TYPE: PRT
C--> 272 <213> ORGANISM: Artificial
     274 <220> FEATURE:
     275 <221> NAME/KEY: MOD_RES
     276 <222> LOCATION: (2)..(2)
     277 <223> OTHER INFORMATION: PHOSPHORYLATION
     280 <400> SEQUENCE: 15
     282 Phe Thr Pro Leu Gln
     283 1               5
     286 <210> SEQ ID NO: 16
     287 <211> LENGTH: 8
     288 <212> TYPE: PRT
C--> 289 <213> ORGANISM: Artificial
     291 <220> FEATURE:
     292 <221> NAME/KEY: MOD_RES
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RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:01

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

293 <222> LOCATION: (4)..(4)
294 <223> OTHER INFORMATION: PHOSPHORYLATION
297 <400> SEQUENCE: 16
299 Arg Lys Arg Thr Leu Arg Arg Leu
300 1 5
303 <210> SEQ ID NO: 17
304 <211> LENGTH: 7
305 <212> TYPE: PRT
C--> 306 <213> ORGANISM: Artificial
308 <220> FEATURE:
309 <221> NAME/KEY: MOD_RES
310 <222> LOCATION: (5)..(5)
311 <223> OTHER INFORMATION: PHOSPHORYLATION
314 <400> SEQUENCE: 17
316 Leu Arg Arg Ala Ser Leu Gly
317 1 5
320 <210> SEQ ID NO: 18
321 <211> LENGTH: 12
322 <212> TYPE: PRT
C--> 323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <221> NAME/KEY: MOD_RES
327 <222> LOCATION: (8)..(8)
328 <223> OTHER INFORMATION: PHOSPHORYLATION
331 <400> SEQUENCE: 18
333 Lys Lys Leu Asn Arg Thr Leu Ser Val Ala Ser Leu
334 1 5 10
337 <210> SEQ ID NO: 19
338 <211> LENGTH: 7
339 <212> TYPE: PRT
C--> 340 <213> ORGANISM: Artificial
342 <220> FEATURE:
343 <221> NAME/KEY: MOD_RES
344 <222> LOCATION: (6)..(6)
345 <223> OTHER INFORMATION: PHOSPHORYLATION
348 <220> FEATURE:
349 <221> NAME/KEY: MOD_RES
350 <222> LOCATION: (7)..(7)
351 <223> OTHER INFORMATION: AMIDATION
354 <400> SEQUENCE: 19
356 Arg Pro Arg Ala Ala Thr Phe
357 1 5
360 <210> SEQ ID NO: 20
361 <211> LENGTH: 7
362 <212> TYPE: PRT
C--> 363 <213> ORGANISM: Artificial
365 <220> FEATURE:
366 <221> NAME/KEY: MOD_RES
367 <222> LOCATION: (5)..(5)

VERIFICATION SUMMARY DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:02

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:47 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:74 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:76 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:76 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:85 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:87 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:87 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:96 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:98 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:98 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:124 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:141 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:164 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:181 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:198 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:238 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
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L:421 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:462 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:497 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:520 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:537 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:566 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:601 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:630 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:647 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:664 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:681 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:698 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:715 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:717 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:717 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:726 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:728 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:728 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:737 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:739 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:739 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

VERIFICATION SUMMARY DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444 TIME: 14:32:02

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

L:748 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:750 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:750 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:759 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:761 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:761 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:770 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:772 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:772 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:781 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:783 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:783 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:792 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:794 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:794 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:803 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:805 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:805 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:814 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:816 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:816 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:825 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:827 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:827 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:836 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:838 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:838 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:847 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:849 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:849 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:858 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:875 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48